

SEQLIST.TXT
SEQUENCE LISTING

<110> Iourgenko, Vadim
Labow, Mark A.
Song, Chuanzheng
Zhang, Wenjun
Zhu, Jian

<120> Cyclic AMP Response Element Activator
Proteins and Uses Related Thereto

<130> 4-32999P2

<150> 60/463,934

<151> 2003-04-18

<160> 39

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<211> 2878

<212> DNA

<213> human

<400> 1

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SEQLIST.TXT

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 <213> human

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 Gln Tyr Leu Gln Leu Gly Pro Ser Arg Gly Gln Tyr Tyr Gly Gly Ser
 50 55 60
 Leu Pro Asn Val Asn Gln Ile Gly Ser Gly Thr Met Asp Leu Pro Phe
 65 70 75 80
 Gln Pro Ser Gly Phe Leu Gly Glu Ala Leu Ala Ala Ala Pro Val Ser
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 Leu Thr Pro Phe Gln Ser Ser Gly Leu Asp Thr Ser Arg Thr Thr Arg
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 Ser Trp Arg Arg Thr Asn Ser Asp Ser Ala Leu His Gln Ser Thr Met
 165 170 175
 Thr Pro Thr Gln Pro Glu Ser Phe Ser Ser Gly Ser Gln Asp Val His
 180 185 190
 Gln Lys Arg Val Leu Leu Leu Thr Val Pro Gly Met Glu Glu Thr Thr
 195 200 205
 Ser Glu Ala Asp Lys Asn Leu Ser Lys Gln Ala Trp Asp Thr Lys Lys
 210 215 220
 Thr Gly Ser Arg Pro Lys Ser Cys Glu Val Pro Gly Ile Asn Ile Phe
 225 230 235 240
 Pro Ser Ala Asp Gln Glu Asn Thr Thr Ala Leu Ile Pro Ala Thr His
 245 250 255 260
 Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn Ile His Phe Pro Ser
 265 270 275
 Pro Leu Pro Thr Pro Leu Asp Pro Glu Glu Pro Thr Phe Pro Ala Leu
 280 285
 Ser Ser Ser Ser Thr Gly Asn Leu Ala Ala Asn Leu Thr His Leu
 290 295 300
 Gly Ile Gly Gly Ala Gly Gln Gly Met Ser Thr Pro Gly Ser Ser Pro
 305 310 315 320
 Gln His Arg Pro Ala Gly Val Ser Pro Leu Ser Leu Ser Thr Glu Ala
 325 330 335
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 340 345 350
 Gln Ala Val Ala Met Asp Ala Leu Ser Leu Glu Gln Gln Leu Pro Tyr
 355 360 365
 Ala Phe Phe Thr Gln Ala Gly Ser Gln Gln Pro Pro Pro Gln Pro Gln
 370 375 380
 Pro Pro Pro Pro Pro Pro Ala Ser Gln Gln Pro Pro Pro Pro Pro
 385 390 395 400
 Pro Pro Gln Ala Pro Val Arg Leu Pro Pro Gly Gly Pro Leu Leu Pro
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SEQLIST.TXT

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Asn Gln Gly Phe Ser Pro Gly Ser Ser Pro Gln His Thr Ser Thr Leu
Gly Ser Val Phe Gly Asp Ala Tyr Tyr Glu Gln Gln Met Ala Ala Arg
Gln Ala Asn Ala Leu Ser His Gln Leu Glu Gln Phe Asn Met Met Glu
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Tyr Ser Gln Ala Ala Met Met Gly Leu Thr Gly Ser His Gly Ser Leu
Pro Asp ser Gln Gln Leu Gly Tyr Ala Ser His Ser Gly Ile Pro Asn
Ile Ile Leu Thr Val Thr Gly Glu Ser Pro Pro Ser Leu Ser Lys Glu
Leu Thr ser Ser Leu Ala Gly Val Gly Asp Val Ser Phe Asp Ser Asp
Ser Gln Phe Pro Leu Asp Glu Leu Lys Ile Asp Pro Leu Thr Leu Asp
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Thr Glu Asp Thr Phe Arg Met Asp Arg Leu

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32

<210> 4
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<220>
 <223> primer

<400> 4
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23

<210> 5
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 <212> DNA
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<220>
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36

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SEQLIST.TXT

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<223> primer

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<210> 8
<211> 39
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<213> Artificial Sequence

<220>
<223> primer

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SEQLIST.TXT

<223> primer

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19

<210> 13

<211> 19

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<223> primer

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<213> Artificial Sequence

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<223> primer

<400> 14

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<210> 15

<211> 2520

<212> DNA

<213> human

<220>

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<221> misc_feature

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2505, 2512, 2514, 2519, 2520

<223> n = A,T,C or G

<400> 15

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SEQLIST.TXT

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 <212> PRT
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 35 40 45
 Ser Thr Arg Leu Gln Ala Gln Lys Leu Arg Leu Ala Tyr Thr Arg Ser
 50 55 60
 Ser His Tyr Gly Gly Ser Leu Pro Asn Val Asn Gln Ile Gly Ser Gly
 65 70 75 80
 Leu Ala Glu Phe Gln Ser Pro Leu His Ser Pro Leu Asp Ser Ser Arg
 85 90 95
 Ser Thr Arg His Gly Leu Val Glu Arg Val Gln Arg Asp Pro Arg
 100 105 110
 Arg Met Val Ser Pro Leu Arg Arg Tyr Thr Arg His Ile Asp Ser Ser
 115 120 125
 Pro Tyr Ser Pro Ala Tyr Leu Ser Pro Pro Pro Glu Ser Ser Trp Arg
 130 135 140
 Arg Thr Met Ala Trp Gly Asn Phe Pro Ala Glu Lys Gly Gln Leu Phe
 145 150 155 160
 Arg Leu Pro Ser Ala Leu Asn Arg Thr Ser Asp Ser Ala Leu His
 165 170 175
 Thr Ser Val Met Asn Pro Ser Pro Gln Asp Thr Tyr Pro Gly Pro Thr
 180 185 190
 Pro Pro Ser Ile Leu Pro Ser Arg Arg Gly Gly Ile Leu Asp Gly Glu
 195 200 205
 Met Asp Pro Lys Val Pro Ala Ile Glu Glu Asn Leu Leu Asp Asp Lys
 210 215 220
 His Leu Leu Lys Pro Trp Asp Ala Lys Lys Leu Ser Ser Ser Ser Ser
 225 230 235 240
 Arg Pro Arg Ser Cys Glu Val Pro Gly Ile Asn Ile Phe Pro Ser Pro
 245 250 255
 Asp Gln Pro Ala Asn Val Pro Val Leu Pro Pro Ala Met Asn Thr Gly
 260 265 270
 Gly Ser Leu Pro Asp Leu Thr Asn Leu His Phe Pro Pro Leu Pro
 275 280 285
 Thr Pro Leu Asp Pro Glu Glu Thr Ala Tyr Pro Ser Leu Ser Gly Gly
 290 295 300
 Asn Ser Thr Ser Asn Leu Thr His Thr Met Thr His Leu Gly Ile Ser
 305 310 315 320
 Arg Gly His Gly Pro Gly Pro Gly Tyr Asp Ala Pro Gly Leu His Ser
 325 330 335
 Pro Leu Ser His Pro Ser Leu Gln Ser Ser Leu Ser Asn Pro Asn Leu

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Thr Ser Leu Gly His Pro Ser Leu Ser Ala Pro Ala Leu Ser Ser Ser
      385      390      400
Ser Ser Ser Ser Ser Thr Ser Ser Pro Val Leu Gly Ala Pro Ser Tyr
      405      410      415
Pro Ala Ser Thr Pro Gly Ala Ser Pro His His Arg Arg Val Pro Leu
      420      425      430
Ser Pro Leu Ser Leu Leu Ala Gly Pro Ala Asp Ala Arg Arg Ser Gln
      435      440      445
Gln Gln Leu Pro Lys Gln Phe Ser Pro Thr Met Ser Pro Thr Leu Ser
      450      455      460
Ser Ile Thr Gln Gly Val Pro Leu Asp Thr Ser Lys Leu Ser Thr Asp
      465      470      475
Gln Arg Leu Pro Tyr Pro Tyr Ser Ser Pro Ser Leu Val Leu Pro
      485      490      495
Thr Gln Pro His Thr Pro Lys Ser Leu Gln Gln Pro Gly Leu Pro Ser
      500      505      510
Gln Ser Cys Ser Val Gln Ser Ser Gly Gly Gln Pro Pro Gly Arg Gln
      515      520      525
Ser His Tyr Gly Thr Pro Tyr Pro Pro Gly Pro Ser Gly His Gly Gln
      530      535      540
Gln Ser Tyr His Arg Pro Met Ser Asp Phe Asn Leu Gly Asn Leu Glu
      545      550      555
Gln Phe Ser Met Glu Ser Pro Ser Ala Ser Leu Val Leu Asp Pro Pro
      565      570      575
Gly Phe Ser Glu Gly Pro Gly Phe Leu Gly Gly Glu Gly Pro Met Gly
      580      585      590
Gly Pro Gln Asp Pro His Thr Phe Asn His Gln Asn Leu Thr His Cys
      595      600      605
Ser Arg His Gly Ser Gly Pro Asn Ile Ile Leu Thr Gly Asp Ser Ser
      610      615      620
Pro Gly Phe Ser Lys Glu Ile Ala Ala Ala Leu Ala Gly Val Pro Gly
      625      630      635
Phe Glu Val Ser Ala Ala Gly Leu Glu Leu Gly Leu Gly Leu Glu Asp
      645      650      655
Glu Leu Arg Met Glu Pro Leu Gly Leu Glu Gly Leu Asn Met Leu Ser
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Asp Pro Cys Ala Leu Leu Pro Asp Pro Ala Val Glu Glu Ser Phe Arg
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Ser Asp Arg Leu Gln
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 <212> DNA
 <213> human

<400> 17
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17

<210> 18
 <211> 7
 <212> PRT
 <213> human

<400> 18
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<210> 19
 <211> 7
 <212> PRT

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<213> unknown

<220>

<223> predicted protein

<400> 19

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<210> 20

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 20

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<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 21

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<210> 22

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 22

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<210> 23

<211> 63

<212> DNA

<213> Artificial Sequence

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<223> primer

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<210> 24

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<213> human

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<221> misc_feature

<222> 1, 13

<223> n = A,T,C or G

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SEQLIST.TXT

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gaactgcagg actcttttca tttgagacca agcccgtatt ccaactgcgg gagtctccc 1680
aacaccatcc tgccagaaga ctccagcacc agcctgttca aagacctcaa cagtgcgctg 1740
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accacgggct ttcgttatct tgacatagaa ggaagcagtg ccacggctcc aggggtttcag 2040
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cccgcctgtg gccaaagtcg tgttgagca ggcaggctgc ttggagcttc ccatgaactg 2160
gaaagctcac ctccactgca tctttttact ggccatccag tcagccgatg tgtaagagta 2220
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<210> 25
 <211> 619
 <212> PRT
 <213> human

<400> 25
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 20 25 30
 Phe Glu Gln Leu Met Thr Asp Leu Thr Leu Ser Arg Val Gln Phe Gln
 35 40 45
 Lys Leu Gln Gln Leu Arg Leu Thr Gln Tyr His Gly Ser Leu Pro
 50 55 60
 Asn Val Ser Gln Leu Arg Ser Asn Ala Ser Glu Phe Gln Pro Ser Phe
 65 70 75 80
 His Gln Ala Asp Asn Val Arg Gly Thr Arg His His Gly Leu Val Glu
 85 90 95
 Arg Pro Ser Arg Asn Arg Phe His Pro Leu His Arg Arg Ser Gly Asp
 100 105 110
 Lys Pro Gly Arg Gln Phe Asp Gly Ser Ala Phe Gly Ala Asn Tyr Ser
 115 120 125
 Ser Gln Pro Leu Asp Glu Ser Trp Pro Arg Gln Gln Pro Pro Trp Lys
 130 135 140
 Asp Glu Lys His Pro Gly Phe Arg Leu Thr Ser Ala Leu Asn Arg Thr
 145 150 155 160
 Asn Ser Asp Ser Ala Leu His Thr Ser Ala Leu Ser Thr Lys Pro Gln
 165 170 175
 Asp Pro Tyr Gly Gly Gly Gly Gln Ser Ala Trp Pro Ala Pro Tyr Met
 180 185 190
 Gly Phe Cys Asp Gly Glu Asn Asn Gly His Gly Glu Val Ala Ser Phe

SEQLIST.TXT

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195      200      205
Pro Gly Pro Leu Lys Glu Glu Asn Leu Leu Asn Val Pro Lys Pro Leu
210      215      220
Pro Lys Gln Leu Trp Glu Thr Lys Glu Ile Gln Ser Leu Ser Gly Arg
225      230      235
Pro Arg Ser Cys Asp Val Gly Gly Gly Asn Ala Phe Pro His Asn Gly
245      250      255
Gln Asn Leu Gly Leu Ser Pro Phe Leu Gly Thr Leu Asn Thr Gly Gly
260      265      270
Ser Leu Pro Asp Leu Thr Asn Leu His Tyr Ser Thr Pro Leu Pro Ala
275      280      285
Ser Leu Asp Thr Thr Asp His His Phe Gly Ser Met Ser Val Gly Asn
290      295      300
Ser Val Asn Asn Ile Pro Ala Ala Met Thr His Leu Gly Ile Arg Ser
305      310      315
Ser Ser Gly Leu Gln Ser Ser Arg Ser Asn Pro Ser Ile Gln Ala Thr
325      330      335
Leu Asn Lys Thr Val Leu Ser Ser Ser Leu Asn Asn His Pro Gln Thr
340      345      350
Ser Val Pro Asn Ala Ser Ala Leu His Pro Ser Leu Arg Leu Phe Ser
355      360      365
Leu Ser Asn Pro Ser Leu Ser Thr Thr Asn Leu Ser Gly Pro Ser Arg
370      375      380
Arg Arg Gln Pro Pro Val Ser Pro Leu Thr Leu Ser Pro Gly Pro Glu
385      390      395
Ala His Gln Gly Phe Ser Arg Gln Leu Ser Thr Ser Pro Leu Ala
405      410      415
Pro Tyr Pro Thr Ser Gln Met Val Ser Ser Asp Arg Ser Gln Leu Ser
420      425      430
Phe Leu Pro Thr Glu Ala Gln Ala Gln Val Ser Pro Pro Pro Tyr
435      440      445
Pro Ala Pro Gln Glu Leu Thr Gln Pro Leu Leu Gln Gln Pro Arg Ala
450      455      460
Pro Glu Ala Pro Ala Gln Gln Pro Gln Ala Ala Ser Ser Leu Pro Gln
465      470      475
Ser Asp Phe Gln Leu Pro Ala Gln Gly Ser Ser Leu Thr Asn Phe
485      490      495
Phe Pro Asp Val Gly Phe Asp Gln Gln Ser Met Arg Pro Gly Pro Ala
500      505      510
Phe Pro Gln Val Pro Leu Val Gln Gln Gly Ser Arg Glu Leu Gln
515      520      525
Asp Ser Phe His Leu Arg Pro Ser Pro Tyr Ser Asn Cys Gly Ser Leu
530      535      540
Pro Asn Thr Ile Leu Pro Glu Asp Ser Ser Thr Ser Leu Phe Lys Asp
545      550      555
Leu Asn Ser Ala Leu Ala Gly Leu Pro Glu Val Ser Leu Asn Val Asp
565      570      575
Thr Pro Phe Pro Leu Glu Glu Glu Leu Gln Ile Glu Pro Leu Ser Leu
580      585      590
Asp Gly Leu Asn Met Leu Ser Asp Ser Ser Met Gly Leu Leu Asp Pro
595      600      605
Ser Val Glu Glu Thr Phe Arg Ala Asp Arg Leu
610      615

```

<210> 26
 <211> 2992
 <212> DNA
 <213> drosophila melanogaster

<400> 26
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 cctgcgaatc agaagatcct agacggcctt gtcggcggtc aggaggtaag ccaatcctcg 180
 ccaggcgcag gcaatgggac gggcggaggt ggcagtgtt ccggcagtgg agccagcggc 240
 ggaggagcct caccagatgg cctgggagggc ggcgggtggt ctccgacggc ttatcgagaa 300
 tcccggagggc gcagcgtagg tgtgggtccc atgcgaagac cgctcgagcg caagcaggat 360
 cgttcgccct acggcagcag cagtacgcaa caaaccttag acaacggcca gctaaatccg 420

SEQLIST.TXT

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catcttcttg gtccacctac ggccggagagt ttgtggcggc ggtccagctc cgattcggcg 480
ctgcaccaa gtgcgctggt ggccgggcttc aatagcgacg tgaactcgat gggcgccaac 540
tatcagcagc agcaacatca gcaacaacag caaccgggccc agccaagatc tcactcgccg 600
caccatggta taaacaggac catgagtccg caggcgcaac ggaggaagtc gccgctactg 660
cagccccatc agctgcagtt gcagcaactg caacagcagc agcaacagat gcaacatcag 720
catcagctgc accagcagct ccaaatgcag cagctgcaac agcaccagca gcaacaccag 780
cagcagcagc aacaacagaa cacgccatac aacaacgcca aattcacgaa tcctgtgttc 840
cggccgctgc aggatcaggt caactttgcc aacaccggct ccctgcccga tctcacggcc 900
cttcaaaact atggacccca gcagcagcag cagcaatccc agcaacagcc gtcgcagcaa 960
caacagcagt tgcagcaaac cctgtcgcca gtcagtgtctc cgcacaatca ccgcccgaa 1020
cgggatcagt cgcccagtcg gtttagtccg gcgggtggag gagggggagc aggtcccggg 1080
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ggttacaaca agccggagat gttggacttc agcagagctga gcggcagccc ggaggcgagt 1680
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gggtgtggtg gatccacgca caacggcagc acaaatctaa atggagcggg aaacaacaat 1800
agcagtagtg gaggtggcac ggccgaggat cctttgggaa taaccacttc gcctgtgccc 1860
tcacccttgg gctgccccag ttcaccgctg ccgataccga ttccgatgtc ggccgaaagc 1920
tcgccacagc agcagcacca ccatcatcag cagcagcaac aacagcatca tcagcagcaa 1980
caccatcagc agcagcaatt atcattatct tgcaccatt cgccgcatca ttcgccaatg 2040
cattcgccgc accatgggaa ttcaccgctt tcaagcagct cgccagttag tcacaatgcc 2100
tgctccaact ccaacgtggt gatgaaccac cagcagcagc agcaacaaca tcaccaccag 2160
caacaccatc atcagggctc ctgcgcaaagt cacacgccga ccacagcgaa tataccctct 2220
attatcttta gtgattactc ctccaacgcg gattatacca gggagatctt cgactccctc 2280
gatctggatc tgggacagat ggacgtagcc gttttgcaga tgctgtccga ccagacccc 2340
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gcagcagtag taacagttga agaggcagcc acagttagcg agaaggacaa aaaagattg 2580
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gacgaggaag tgcgcaattt ctttttttag gcagccagca agtcattttt gtcgttaaca 2700
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acaaattcac ttccgcaaat tcatgctgaa actgaaagtt ttctaacagt cctcaatatt 2940
gttatctcgt tatcgtccgt gctttcgtag ctagtctcta caacaaaaat ac 2992

```

<210> 27
 <211> 797
 <212> PRT
 <213> drosophila melanogaster

<400> 27
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 Lys Gln Ala Glu Gly Thr Ala Glu Phe Glu Arg Ile Met Lys Glu Val
 20 25 30
 Tyr Ala Thr Lys Arg Asp Glu Pro Ala Asn Gln Lys Ile Leu Asp
 35 40 45
 Gly Leu Val Gly Gly Gln Glu Val Ser Gln Ser Ser Pro Gly Ala Gly
 50 55 60
 Asn Gly Thr Gly Gly Gly Ser Gly Ser Gly Ser Gly Ala Ser Gly
 65 70 75 80
 Gly Gly Ala Ser Pro Asp Gly Leu Gly Gly Gly Gly Ser Pro Thr
 85 90 95
 Ala Tyr Arg Glu Ser Arg Gly Arg Ser Val Gly Val Gly Pro Met Arg
 100 105 110
 Arg Pro Ser Glu Arg Lys Gln Asp Arg Ser Pro Tyr Gly Ser Ser Ser
 115 120 125
 Thr Gln Gln Thr Leu Asp Asn Gly Gln Leu Asn Pro His Leu Leu Gly
 130 135 140

SEQLIST.TXT

```

Pro  Pro  Thr  Ala  Glu  Ser  Leu  Trp  Arg  Arg  Ser  Ser  Ser  Asp  Ser  Ala
145 150 155 160
Leu  His  Gln  Ser  Ala  Leu  Val  Ala  Gly  Phe  Asn  Ser  Asp  Val  Asn  Ser
165 170 175
Met  Gly  Ala  Asn  Tyr  Gln  Gln  Gln  Gln  His  Gln  Gln  Gln  Gln  Gln  Pro
180 185 190
Gly  Gln  Pro  Arg  Ser  His  Ser  Pro  His  His  Gly  Ile  Asn  Arg  Thr  Met
195 200 205
Ser  Pro  Gln  Ala  Gln  Arg  Arg  Lys  Ser  Pro  Leu  Leu  Gln  Pro  His  Gln
210 215 220
Leu  Gln  Leu  Gln  Gln  Leu  Gln  Gln  Gln  Gln  Gln  Gln  Met  Gln  His  Gln
225 230 235 240
His  Gln  Leu  His  Gln  Gln  Leu  Gln  Met  Gln  Gln  Leu  Gln  Gln  His  Gln
245 250 255
Gln  Gln  His  Gln  Gln  Gln  Gln  Gln  Gln  Gln  Asn  Thr  Pro  Tyr  Asn  Asn
260 265 270
Ala  Lys  Phe  Thr  Asn  Pro  Val  Phe  Arg  Pro  Leu  Gln  Asp  Gln  Val  Asn
275 280 285
Phe  Ala  Asn  Thr  Gly  Ser  Leu  Pro  Asp  Leu  Thr  Ala  Leu  Gln  Asn  Tyr
290 295 300
Gly  Pro  Gln  Gln  Gln  Gln  Gln  Gln  Ser  Gln  Gln  Gln  Pro  Ser  Gln  Gln
305 310 315 320
Gln  Gln  Gln  Leu  Gln  Gln  Thr  Leu  Ser  Pro  Val  Met  Ser  Pro  His  Asn
325 330 335
His  Arg  Arg  Glu  Arg  Asp  Gln  Ser  Pro  Ser  Pro  Phe  Ser  Pro  Ala  Gly
340 345 350
Gly  Gly  Gly  Gly  Ala  Gly  Pro  Gly  Ser  Pro  Tyr  Gln  Gln  Gln  His
355 360 365
Ser  Pro  Thr  Gly  Asn  Thr  Gln  Gln  Gln  Gln  Gln  Gln  His  Gln  Gln  Pro
370 375 380
Ser  Asn  Ser  Pro  His  Leu  Ser  Phe  Thr  Asn  Leu  Ala  Thr  Thr  Gln  Ala
385 390 395 400
Ala  Val  Thr  Thr  Phe  Asn  Pro  Leu  Pro  Thr  Leu  Gly  Pro  His  Asn  Ala
405 410 415
Thr  Asp  Tyr  Arg  Gln  Pro  Pro  Asn  Pro  Pro  Ser  Pro  Arg  Ser  Ser  Pro
420 425 430
Gly  Leu  Leu  Ser  Ser  Val  Ser  Ala  Thr  Asp  Leu  His  Ser  Ser  Ala  Pro
435 440 445
Ala  Ser  Pro  Ile  Arg  Gln  Gln  Gln  Gln  Ala  His  Gln  Gln  Gln  Gln  Gln
450 455 460
Gln  Gln  Gln  Ala  Gln  Gln  Gln  Gln  Gln  Phe  Asp  Asn  Ser  Tyr  Asn
465 470 475 480
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485 490 495
Asp  Ser  Asn  Ser  Ser  Pro  Glu  Gln  Gln  Gly  Phe  Ala  Asn  Asn  Phe  Val
500 505 510
Ala  Leu  Asp  Phe  Asp  Asp  Leu  Ser  Gly  Gly  Gly  Gly  Gly  Gly  Pro  Ser
515 520 525
Gly  Gly  Gly  Gly  Ser  Asn  Gly  Gly  Leu  Thr  Asn  Gly  Tyr  Asn  Lys
530 535 540
Pro  Glu  Met  Leu  Asp  Phe  Ser  Glu  Leu  Ser  Gly  Ser  Pro  Glu  Ala  Ser
545 550 555 560
Gly  Asn  Asn  Asn  His  Met  Arg  Arg  Gly  Val  Ser  Asn  Leu  Asn  Asn  Asn
565 570 575
Gly  Leu  Ser  Asn  Gly  Val  Val  Gly  Ser  Thr  His  Asn  Gly  Ser  Thr  Asn
580 585 590
Leu  Asn  Gly  Ala  Gly  Asn  Asn  Asn  Ser  Ser  Ser  Gly  Gly  Gly  Thr  Ala
595 600 605
Gln  Asp  Pro  Leu  Gly  Ile  Thr  Thr  Ser  Pro  Val  Pro  Ser  Pro  Leu  Gly
610 615 620
Cys  Pro  Ser  Ser  Pro  Leu  Pro  Ile  Pro  Ile  Pro  Met  Ser  Ala  Gln  Ser
625 630 635 640
Ser  Pro  Gln  Gln  Gln  His  His  His  His  Gln  Gln  Gln  Gln  Gln  His
645 650 655
His  Gln  Gln  Gln  His  His  Gln  Gln  Gln  Gln  Leu  Ser  Leu  Ser  Leu  His
660 665 670
His  Ser  Pro  His  His  Ser  Pro  Met  His  Ser  Pro  His  His  Gly  Asn  Ser
675 680 685

```

SEQLIST.TXT

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Pro Leu Ser Ser Ser Ser Pro Val Ser His Asn Ala Cys Ser Asn Ser
  690      695      700
Asn Val Val Met Asn His Gln Gln Gln Gln Gln His His His Gln
  705      710      715
Gln His His His Gln Gly Ser Ser Gln Ser His Thr Pro Thr Thr Ala
  725      730      735
Asn Ile Pro Ser Ile Ile Phe Ser Asp Tyr Ser Ser Asn Ala Asp Tyr
  740      745      750
Thr Arg Glu Ile Phe Asp Ser Leu Asp Leu Gly Gln Met Asp
  755      760      765
Val Ala Gly Leu Gln Met Leu Ser Asp Gln Asn Pro Ile Met Ile Ala
  770      775      780
Asp Pro Asn Ile Glu Asp Ser Phe Arg Arg Asp Leu Asn
  785      790      795

```

```

<210> 28
<211> 2416
<212> DNA
<213> mouse

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```

<220>
<221> misc_feature
<222> 1528
<223> n = A,T,C or G

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```

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cgaggagggtc atgaaggacc tgagcctgac gcggggccgc cggcttcagc tgcagaagtc 180
ccagtacctg cagctgggcc ccagccgtgg ccagtactac ggtgggtccc tgcccaacgt 240
gaaccagatt ggaagcagca gcgtggacct ggccttccag accccatttc agtcctcagg 300
cctggacacg agtcggacca cagcacatca tgggcttggt gacagagtat atcgtgagcg 360
tggcagactt ggctccccgc accgtcgacc cctgtcagta gacaagcatg ggcgacaggc 420
tgacagctgc ccctatggca ccgtgtacct ctgcctcctt gcggacacca gctggaggag 480
gaccaactct gactctgccc tgcaccagag cacaatgaca ccagccagg cagagtcctt 540
cacaggcggg tcccaggatg cgcaccagaa gagagtctta ctgctaactg tcccaggaa 600
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ggcgggttcc aggcccaagt cctgtgaggt ccccggaatc aacatctttc cgtctgcaga 720
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tcccaccgac atccct

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SEQLIST.TXT

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 <211> 629
 <212> PRT
 <213> mouse

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 Lys Asp Leu Ser Leu Thr Arg Ala Ala Arg Leu Gln Leu Gln Lys Ser
 35 40 45
 Gln Tyr Leu Gln Leu Gly Pro Ser Arg Gly Gln Tyr Tyr Gly Gly Ser
 50 55 60
 Leu Pro Asn Val Asn Gln Ile Gly Ser Ser Ser Val Asp Leu Ala Phe
 65 70 75 80
 Gln Thr Pro Phe Gln Ser Ser Gly Leu Asp Thr Ser Arg Thr Thr Arg
 85 90 95
 His His Gly Leu Val Asp Arg Val Tyr Arg Glu Arg Gly Arg Leu Gly
 100 105 110
 Ser Pro His Arg Arg Pro Leu Ser Val Asp Lys His Gly Arg Gln Ala
 115 120 125
 Asp Ser Cys Pro Tyr Gly Thr Val Tyr Leu Ser Pro Pro Ala Asp Thr
 130 135 140
 Ser Trp Arg Arg Thr Asn Ser Asp Ser Ala Leu His Gln Ser Thr Met
 145 150 155 160
 Thr Pro Ser Gln Ala Glu Ser Phe Thr Gly Gly Ser Gln Asp Ala His
 165 170 175
 Gln Lys Arg Val Leu Leu Leu Thr Val Pro Gly Met Glu Asp Thr Gly
 180 185 190
 Ala Glu Thr Asp Lys Thr Leu Ser Lys Gln Ser Trp Asp Ser Lys Lys
 195 200 205
 Ala Gly Ser Arg Pro Lys Ser Cys Glu Val Pro Gly Ile Asn Ile Phe
 210 215 220
 Pro Ser Ala Asp Gln Glu Asn Thr Thr Ala Leu Ile Pro Ala Thr His
 225 230 235 240
 Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn Ile His Phe Ala Ser
 245 250 255
 Pro Leu Pro Thr Pro Leu Asp Pro Glu Pro Pro Phe Pro Ala Leu
 260 265 270
 Thr Ser Ser Ser Ser Thr Gly Ser Leu Ala His Leu Gly Val Gly Gly
 275 280 285
 Ala Gly Gly Met Asn Thr Pro Ser Ser Ser Pro Gln His Arg Pro Ala
 290 295 300
 Val Val Ser Pro Leu Ser Leu Ser Thr Glu Ala Arg Arg Gln Gln Ala
 305 310 315 320
 Gln Gln Val Ser Pro Thr Leu Ser Pro Leu Ser Pro Ile Thr Gln Ala
 325 330 335
 Val Ala Met Asp Ala Leu Ser Leu Glu Gln Gln Leu Pro Tyr Ala Phe
 340 345 350
 Phe Thr Gln Thr Gly Ser Gln Gln Pro Pro Pro Gln Pro Gln Pro Pro
 355 360 365
 Pro Pro Pro Pro Val Ser Gln Gln Gln Pro Pro Pro Gln Val
 370 375 380
 Ser Val Gly Leu Pro Gln Gly Gly Pro Leu Leu Pro Ser Ala Ser Leu
 385 390 395 400
 Thr Arg Gly Pro Gln Leu Pro Pro Leu Ser Val Thr Val Pro Ser Thr
 405 410 415
 Leu Pro Gln Ser Pro Thr Glu Asn Pro Gly Gln Ser Pro Met Gly Ile
 420 425 430
 Asp Ala Thr Ser Ala Pro Ala Leu Gln Tyr Arg Thr Ser Ala Gly Ser
 435 440 445
 Pro Ala Thr Gln Ser Pro Thr Ser Pro Val Ser Asn Gln Gly Phe Ser
 450 455 460
 Pro Gly Ser Ser Pro Gln His Thr Ser Thr Leu Gly Ser Val Phe Gly
 465 470 475 480
 Asp Ala Tyr Tyr Glu Gln Gln Met Thr Ala Arg Gln Ala Asn Ala Leu

SEQLIST.TXT

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      485      490      495
Ser Arg Gln Leu Glu Gln Phe Asn Met Met Glu Asn Ala Ile Ser Ser
      500      505      510
Ser Ser Leu Tyr Asn Pro Gly Ser Thr Leu Asn Tyr Ser Gln Ala Ala
      515      520      525
Met Met Gly Leu Ser Gly Ser His Gly Gly Leu Gln Asp Pro Gln Gln
      530      535      540
Leu Gly Tyr Thr Gly His Gly Gly Ile Pro Asn Ile Ile Leu Thr Val
      545      550      555      560
Thr Gly Glu Ser Pro Pro Ser Leu Ser Lys Glu Leu Ser Ser Thr Leu
      565      570      575
Ala Gly Val Ser Asp Val Ser Phe Asp Ser Asp His Gln Phe Pro Leu
      580      585      590
Asp Glu Leu Lys Ile Asp Pro Leu Thr Leu Asp Gly Leu His Met Leu
      595      600      605
Asn Asp Pro Asp Met Val Leu Ala Asp Pro Ala Thr Glu Asp Thr Phe
      610      615      620
Arg Met Asp Arg Leu
      625

```

```

<210> 30
<211> 566
<212> PRT
<213> fugu rubripres

```

```

<400> 30
Met Ala Ser Ser Asn Asn Pro Arg Lys Phe Ser Glu Lys Ile Ala Leu
  1      5      10      15
His Asn Gln Lys Gln Ala Glu Glu Thr Ala Ala Phe Glu Glu Val Met
      20      25      30
Lys Asp Leu Asn Val Thr Arg Ala Ala Arg Leu Gln Leu Gln Lys Thr
      35      40      45
Gln Tyr Leu Gln Leu Gly Gln Asn Arg Gly Gln Tyr Tyr Gly Gly Ser
      50      55      60
Leu Pro Asn Val Asn Gln Ile Gly Asn Gly Asn Ile Asp Leu Pro Phe
      65      70      75      80
Gln Val Ser Asn Ser Val Leu Asp Thr Ser Arg Thr Thr Arg His His
      85      90      95
Gly Leu Val Glu Arg Val Tyr Arg Asp Arg Asn Arg Ile Ser Ser Pro
      100      105      110
His Arg Arg Pro Leu Ser Val Asp Lys His Gly Arg Gln Arg Thr Asn
      115      120      125
Ser Asp Ser Ala Leu His Gln Ser Ala Met Asn Pro Lys Pro His Glu
      130      135      140
Val Phe Ala Gly Gly Ser Gln Glu Leu Gln Pro Lys Arg Leu Leu Leu
      145      150      155      160
Thr Val Pro Gly Thr Glu Lys Ser Glu Ser Asn Ala Asp Lys Asp Ser
      165      170      175
Gln Glu Gln Ser Trp Asp Asp Lys Lys Ser Ile Phe Pro Ser Pro Asp
      180      185      190
Gln Glu Leu Asn Pro Ser Val Leu Pro Ala Ala His Asn Thr Gly Gly
      195      200      205
Ser Leu Pro Asp Leu Thr Asn Ile Gln Phe Pro Pro Pro Leu Ser Thr
      210      215      220
Pro Leu Asp Pro Glu Asp Thr Val Thr Phe Pro Ser Leu Ser Ser Ser
      225      230      235      240
Asn Ser Thr Gly Ser Leu Thr Thr Asn Leu Thr His Leu Gly Ile Ser
      245      250      255
Val Ala Ser His Gly Asn Asn Gly Glu Lys Asn Ile Phe Phe Leu Lys
      260      265      270
Thr Cys Thr Ser Cys Glu Asp Val Tyr Asp Phe Tyr Phe Val Gly Ile
      275      280      285
Pro Thr Ser Ser Gln Thr Thr Met Thr Ala Thr Ala Gln Arg Arg Gln
      290      295      300
Pro Pro Val Val Pro Leu Thr Leu Thr Ser Asp Leu Thr Leu Gln Gln
      305      310      315      320
Ser Pro Gln Gln Leu Ser Pro Thr Leu Ser Ser Pro Ile Asn Ile Thr

```

[illegible]

```
<210> 31
<211> 1602
<212> DNA
<213> fuqu rubripres
```

<400>	31					
atggcgctcct	ctaacaatcc	tgcgaaattt	agcgaaaaaa	tcgcactgca	taaccagaaa	60
caagcagagg	agactgctgc	gttcgaagaa	gtgatgaagg	acctgaacgt	cacaaggggt	120
gcccgggttaa	gacagctgca	gttacagaag	accagtat	tgcaactagg	gcagaatcgt	180
ggacagtagt	atgggaggtc	actgcccagt	gtcaatcaga	tgggaaatgg	caacattgac	240
ctgcctttttc	aggtgagcag	gacaaactca	gactcagctt	tacatcagag	tgccatgaat	300
ccaaagcccc	acgaagtgtt	tgctgggggg	tcgcaggagc	tgcaagccaa	acgagtgtg	360
ctaacagtg	ctggaaccga	aaaatcggaa	tcaaacgcag	acaaagattc	gcaggagcag	420
tcgtgggtag	acaaaaagag	tattttttca	tcaccagacc	aggagttaaa	ccccctcggt	480
ctctccagcg	cgacacaac	ggcgggttcg	ctccccgacc	tgaccaacat	ccagttccct	540
cctccactgt	ccacccct	ggaccccgag	gacaccgtca	ccttcccctc	cctcagctcc	600
tctaacagca	caggcagctc	gactaccaac	cttaccaccc	tgggcatcag	tgtggccagc	660
catggttaata	acggagagaa	aaatatattt	tttttaaaaa	catgcacttc	atgcgaggat	720
gttaaataaat	attacgactt	ttatttttga	gggattccca	cttctcttca	aaccaccatg	780
acagcaacag	cacagcggtc	gcaaccaccc	gtggtcccc	tcaccctcac	ctctgacctg	840
actcttcaac	agtcccccca	gcagctttca	cccacccctc	cctcacccat	taacatcaca	900
cagagcatga	agcttagtgc	tagctaact	tcttccccct	aacagtagcc	caatcacagt	960
ggctcaccag	ccactcagtc	tccaacctcc	ccagttccca	atcaaggctt	ctcccccggt	1020
agctcgcttc	aaccacagca	cattctctgtg	gtgggcagta	tatttgggga	ctccttctat	1080
gatcagcagt	tggctctgag	gcagaccaat	gccctttctc	atcaggtgtg	tgaggacggc	1140
cgcagggttag	aaataacaca	cgtacgtctc	tcacgacttc	acgcgagct	ttgtttttgt	1200
ttttctcagc	tggagcagtt	caatatgata	gagaacccca	tcagctccac	cagcctgtac	1260
aatcagtgct	cgacccttaa	ttatacacag	gcagccatga	tgggcttcac	cgggagcagc	1320
ctgcaggact	cgcagcagct	cggctacggc	aatcacggca	acatcccca	catcatactg	1380
acaatttcag	tcacagggga	gtctccggcg	agcctctcca	aagagctgac	caactcattg	1440
gccggcgctg	gcgacgtcag	ctttgatcca	gacacgcagt	ttcctctgga	cgaagtgaag	1500
atccacccgc	tgaccttggg	cggcctgcac	atgctcaacg	accagacat	ggtgtgtggc	1560
gaccccgcca	cagaggacac	gttcaggatg	gacaggctgt	aa		1602

<210> 32

SEQLIST.TXT

<211> 170
 <212> PRT
 <213> human

<400> 32
 Met Ala Thr Ser Asn Asn Pro Arg Lys Phe Ser Glu Lys Ile Ala Leu
 1 5 10 15
 His Asn Gln Lys Gln Ala Glu Glu Thr Ala Ala Phe Glu Glu Val Met
 20 25 30
 Lys Asp Leu Ser Leu Thr Arg Ala Ala Arg Leu Gln Leu Gln Lys Ser
 35 40 45
 Gln Tyr Leu Gln Leu Gly Pro Ser Arg Gly Gln Tyr Tyr Gly Gly Ser
 50 55 60
 Leu Pro Asn Val Asn Gln Ile Gly Ser Gly Thr Met Asp Leu Pro Phe
 65 70 75 80
 Gln Pro Ser Gly Phe Leu Gly Glu Ala Leu Ala Ala Ala Pro Val Ser
 85 90 95
 Leu Thr Pro Phe Gln Ser Ser Gly Leu Asp Thr Ser Arg Thr Thr Arg
 100 105 110
 His His Gly Leu Val Asp Arg Val Tyr Arg Glu Arg Gly Arg Leu Gly
 115 120 125
 Ser Pro His Arg Arg Pro Leu Ser Val Asp Lys His Gly Arg Gln Ala
 130 135 140
 Asp Ser Cys Pro Tyr Gly Thr Met Tyr Leu Ser Pro Pro Ala Asp Thr
 145 150 155 160
 Ser Trp Arg Arg Thr Asn Ser Asp Ser Ala
 165 170

<210> 33
 <211> 356
 <212> PRT
 <213> human

<400> 33
 Met Ala Thr Ser Asn Asn Pro Arg Lys Phe Ser Glu Lys Ile Ala Leu
 1 5 10 15
 His Asn Gln Lys Gln Ala Glu Glu Thr Ala Ala Phe Glu Glu Val Met
 20 25 30
 Lys Asp Leu Ser Leu Thr Arg Ala Ala Arg Leu Gln Leu Gln Lys Ser
 35 40 45
 Gln Tyr Leu Gln Leu Gly Pro Ser Arg Gly Gln Tyr Tyr Gly Gly Ser
 50 55 60
 Leu Pro Asn Val Asn Gln Ile Gly Ser Gly Thr Met Asp Leu Pro Phe
 65 70 75 80
 Gln Pro Ser Gly Phe Leu Gly Glu Ala Leu Ala Ala Ala Pro Val Ser
 85 90 95
 Leu Thr Pro Phe Gln Ser Ser Gly Leu Asp Thr Ser Arg Thr Thr Arg
 100 105 110
 His His Gly Leu Val Asp Arg Val Tyr Arg Glu Arg Gly Arg Leu Gly
 115 120 125
 Ser Pro His Arg Arg Pro Leu Ser Val Asp Lys His Gly Arg Gln Ala
 130 135 140
 Asp Ser Cys Pro Tyr Gly Thr Met Tyr Leu Ser Pro Pro Ala Asp Thr
 145 150 155 160
 Ser Trp Arg Arg Thr Asn Ser Asp Ser Ala Leu His Gln Ser Thr Met
 165 170 175
 Thr Pro Thr Gln Pro Glu Ser Phe Ser Gly Ser Gln Asp Val His
 180 185 190
 Gln Lys Arg Val Leu Leu Leu Thr Val Pro Gly Met Glu Glu Thr Thr
 195 200 205
 Ser Glu Ala Asp Lys Asn Leu Ser Lys Gln Ala Trp Asp Thr Lys Lys
 210 215 220
 Thr Gly Ser Arg Pro Lys Ser Cys Glu Val Pro Gly Ile Asn Ile Phe
 225 230 235 240
 Pro Ser Ala Asp Gln Glu Asn Thr Thr Ala Leu Ile Pro Ala Thr His
 245 250 255
 Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn Ile His Phe Pro Ser

SEQLIST.TXT

```

                260                265                270
Pro Leu Pro Thr Pro Leu Asp Pro Glu Glu Pro Thr Phe Pro Ala Leu
                275                280                285
Ser Ser Ser Ser Thr Gly Asn Leu Ala Ala Asn Leu Thr His Leu
                290                295                300
Gly Ile Gly Gly Ala Gly Gln Gly Met Ser Thr Pro Gly Ser Ser Pro
305 Gln His Arg Pro Ala Gly Val Ser Pro Leu Ser Leu Ser Thr Glu Ala
                310                315                320
Arg Arg Gln Gln Ala Ser Pro Thr Leu Ser Pro Leu Ser Pro Ile Thr
                325                330                335
Gln Ala Val Ala
                340                345                350
                355

```

<210> 34
 <211> 494
 <212> PRT
 <213> human

```

<400> 34
Met Ala Thr Ser Asn Asn Pro Arg Lys Phe Ser Glu Lys Ile Ala Leu
1 5 10 15
His Asn Gln Lys Gln Ala Glu Glu Thr Ala Ala Phe Glu Glu Val Met
20 25 30
Lys Asp Leu Ser Leu Thr Arg Ala Ala Arg Leu Gln Leu Gln Lys Ser
35 40 45
Gln Tyr Leu Gln Leu Gly Pro Ser Arg Gly Gln Tyr Tyr Gly Gly Ser
50 55 60
Leu Pro Asn Val Asn Gln Ile Gly Ser Gly Thr Met Asp Leu Pro Phe
65 70 75 80
Gln Pro Ser Gly Phe Leu Gly Glu Ala Leu Ala Ala Ala Pro Val Ser
85 90 95
Leu Thr Pro Phe Gln Ser Ser Gly Leu Asp Thr Ser Arg Thr Thr Arg
100 105 110
His His Gly Leu Val Asp Arg Val Tyr Arg Glu Arg Gly Arg Leu Gly
115 120 125
Ser Pro His Arg Arg Pro Leu Ser Val Asp Lys His Gly Arg Gln Ala
130 135 140
Asp Ser Cys Pro Tyr Gly Thr Met Tyr Leu Ser Pro Pro Ala Asp Thr
145 150 155 160
Ser Trp Arg Arg Thr Asn Ser Asp Ser Ala Leu His Gln Ser Thr Met
165 170 175
Thr Pro Thr Gln Pro Glu Ser Phe Ser Gly Ser Gln Asp Val His
180 185 190
Gln Lys Arg Val Leu Leu Leu Thr Val Pro Gly Met Glu Glu Thr Thr
195 200 205
Ser Glu Ala Asp Lys Asn Leu Ser Lys Gln Ala Trp Asp Thr Lys Lys
210 215 220
Thr Gly Ser Arg Pro Lys Ser Cys Glu Val Pro Gly Ile Asn Ile Phe
225 230 235 240
Pro Ser Ala Asp Gln Glu Asn Thr Thr Ala Leu Ile Pro Ala Thr His
245 250 255
Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn Ile His Phe Pro Ser
260 265 270
Pro Leu Pro Thr Pro Leu Asp Pro Glu Glu Pro Thr Phe Pro Ala Leu
275 280 285
Ser Ser Ser Ser Thr Gly Asn Leu Ala Ala Asn Leu Thr His Leu
290 295 300
Gly Ile Gly Gly Ala Gly Gln Gly Met Ser Thr Pro Gly Ser Ser Pro
305 310 315 320
Gln His Arg Pro Ala Gly Val Ser Pro Leu Ser Leu Ser Thr Glu Ala
325 330 335
Arg Arg Gln Gln Ala Ser Pro Thr Leu Ser Pro Leu Ser Pro Ile Thr
340 345 350
Gln Ala Val Ala Met Asp Ala Leu Ser Leu Glu Gln Gln Leu Pro Tyr
355 360 365
Ala Phe Phe Thr Gln Ala Gly Ser Gln Gln Pro Pro Gln Pro Gln

```

SEQLIST.TXT

```

      370      375      380
Pro Pro Pro Pro Pro Pro Pro Ala Ser Gln Gln Pro Pro Pro Pro
385      390      395      400
Pro Pro Gln Ala Pro Val Arg Leu Pro Pro Gly Gly Pro Leu Leu Pro
405      410      415
Ser Ala Ser Leu Thr Arg Gly Pro Gln Pro Pro Pro Leu Ala Val Thr
420      425      430
Val Pro Ser Ser Leu Pro Gln Ser Pro Pro Glu Asn Pro Gly Gln Pro
435      440      445
Ser Met Gly Ile Asp Ile Ala Ser Ala Pro Ala Leu Gln Gln Tyr Arg
450      455      460
Thr Ser Ala Gly Ser Pro Ala Asn Gln Ser Pro Thr Ser Pro Val Ser
465      470      475      480
Asn Gln Gly Phe Ser Pro Gly Ser Ser Pro Gln His Thr Ser
      485      490

```

<210> 35
 <211> 580
 <212> PRT
 <213> human

```

<400> 35
Met Ala Thr Ser Asn Asn Pro Arg Lys Phe Ser Glu Lys Ile Ala Leu
1      5      10      15
His Asn Gln Lys Gln Ala Glu Glu Thr Ala Ala Phe Glu Glu Val Met
20      25      30
Lys Asp Leu Ser Leu Thr Arg Ala Ala Arg Leu Gln Leu Gln Lys Ser
35      40      45
Gln Tyr Leu Gln Leu Gly Pro Ser Arg Gly Gln Tyr Tyr Gly Gly Ser
50      55      60
Leu Pro Asn Val Asn Gln Ile Gly Ser Gly Thr Met Asp Leu Pro Phe
65      70      75      80
Gln Pro Ser Gly Phe Leu Gly Glu Ala Leu Ala Ala Ala Pro Val Ser
85      90      95
Leu Thr Pro Phe Gln Ser Ser Gly Leu Asp Thr Ser Arg Thr Thr Arg
100      105      110
His His Gly Leu Val Asp Arg Val Tyr Arg Glu Arg Gly Arg Leu Gly
115      120      125
Ser Pro His Arg Arg Pro Leu Ser Val Asp Lys His Gly Arg Gln Ala
130      135      140
Asp Ser Cys Pro Tyr Gly Thr Met Tyr Leu Ser Pro Pro Ala Asp Thr
145      150      155      160
Ser Trp Arg Arg Thr Asn Ser Asp Ser Ala Leu His Gln Ser Thr Met
165      170      175
Thr Pro Thr Gln Pro Glu Ser Phe Ser Ser Gly Ser Gln Asp Val His
180      185      190
Gln Lys Arg Val Leu Leu Leu Thr Val Pro Gly Met Glu Glu Thr Thr
195      200      205
Ser Glu Ala Asp Lys Asn Leu Ser Lys Gln Ala Trp Asp Thr Lys Lys
210      215      220
Thr Gly Ser Arg Pro Lys Ser Cys Glu Val Pro Gly Ile Asn Ile Phe
225      230      235      240
Pro Ser Ala Asp Gln Glu Asn Thr Thr Ala Leu Ile Pro Ala Thr His
245      250      255
Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn Ile His Phe Pro Ser
260      265      270
Pro Leu Pro Thr Pro Leu Asp Pro Glu Glu Pro Thr Phe Pro Ala Leu
275      280      285
Ser Ser Ser Ser Ser Thr Gly Asn Leu Ala Ala Asn Leu Thr His Leu
290      295      300
Gly Ile Gly Gly Ala Gly Gln Gly Met Ser Thr Pro Gly Ser Ser Pro
305      310      315      320
Gln His Arg Pro Ala Gly Val Ser Pro Leu Ser Leu Ser Thr Glu Ala
325      330      335
Arg Arg Gln Gln Ala Ser Pro Thr Leu Ser Pro Leu Ser Pro Ile Thr
340      345      350
Gln Ala Val Ala Met Asp Ala Leu Ser Leu Glu Gln Gln Leu Pro Tyr

```

SEQLIST.TXT

```

355      360      365
Ala Phe Phe Thr Gln Ala Gly Ser Gln Gln Pro Pro Pro Gln Pro Gln
370      375      380
Pro Pro Pro Pro Pro Pro Ala Ser Gln Gln Pro Pro Pro Pro Pro
385      390      395      400
Pro Pro Gln Ala Pro Val Arg Leu Pro Pro Gly Gly Pro Leu Leu Pro
405      410      415
Ser Ala Ser Leu Thr Arg Gly Pro Gln Pro Pro Pro Leu Ala Val Thr
420      425      430
Val Pro Ser Ser Leu Pro Gln Ser Pro Pro Glu Asn Pro Gly Gln Pro
435      440      445
Ser Met Gly Ile Asp Ile Ala Ser Ala Pro Ala Leu Gln Gln Tyr Arg
450      455      460
Thr Ser Ala Gly Ser Pro Ala Asn Gln Ser Pro Thr Ser Pro Val Ser
465      470      475      480
Asn Gln Gly Phe Ser Pro Gly Ser Ser Pro Gln His Thr Ser Thr Leu
485      490      495
Gly Ser Val Phe Gly Asp Ala Tyr Tyr Glu Gln Gln Met Ala Ala Arg
500      505      510
Gln Ala Asn Ala Leu Ser His Gln Leu Glu Gln Phe Asn Met Met Glu
515      520      525
Asn Ala Ile Ser Ser Ser Ser Leu Tyr Ser Pro Gly Ser Thr Leu Asn
530      535      540
Tyr Ser Gln Ala Ala Met Met Gly Leu Thr Gly Ser His Gly Ser Leu
545      550      555      560
Pro Asp Ser Gln Gln Leu Gly Tyr Ala Ser His Ser Gly Ile Pro Asn
565      570      575
Ile Ile Leu Thr
580

```

<210> 36
 <211> 481
 <212> PRT
 <213> human

```

<400> 36
Ala Leu His Gln Ser Thr Met Thr Pro Thr Gln Pro Glu Ser Phe Ser
1      5      10      15
Ser Gly Ser Gln Asp Val His Gln Lys Arg Val Leu Leu Leu Thr Val
20      25      30
Pro Gly Met Glu Glu Thr Thr Ser Glu Ala Asp Lys Asn Leu Ser Lys
35      40      45
Gln Ala Trp Asp Thr Lys Lys Thr Gly Ser Arg Pro Lys Ser Cys Glu
50      55      60
Val Pro Gly Ile Asn Ile Phe Pro Ser Ala Asp Gln Glu Asn Thr Thr
65      70      75      80
Ala Leu Ile Pro Ala Thr His Asn Thr Gly Gly Ser Leu Pro Asp Leu
85      90      95
Thr Asn Ile His Phe Pro Ser Pro Leu Pro Thr Pro Leu Asp Pro Glu
100      105      110
Glu Pro Thr Phe Pro Ala Leu Ser Ser Ser Ser Thr Gly Asn Leu
115      120      125
Ala Ala Asn Leu Thr His Leu Gly Ile Gly Gly Ala Gly Gln Gly Met
130      135      140
Ser Thr Pro Gly Ser Ser Pro Gln His Arg Pro Ala Gly Val Ser Pro
145      150      155      160
Leu Ser Leu Ser Thr Glu Ala Arg Arg Gln Ala Ser Pro Thr Leu
165      170      175
Ser Pro Leu Ser Pro Ile Thr Gln Ala Val Ala Met Asp Ala Leu Ser
180      185      190
Leu Glu Gln Gln Leu Pro Tyr Ala Phe Phe Thr Gln Ala Gly Ser Gln
195      200      205
Gln Pro Pro Pro Gln Pro Gln Pro Pro Pro Pro Pro Pro Ala Ser
210      215      220
Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Ala Pro Val Arg Leu Pro
225      230      235      240
Pro Gly Gly Pro Leu Leu Pro Ser Ala Ser Leu Thr Arg Gly Pro Gln

```

SEQLIST.TXT

Pro	Pro	Pro	Leu	245	Ala	Val	Thr	Val	Pro	250	Ser	Ser	Leu	Pro	Gln	255	Ser	Pro
Pro	Glu	Asn	260	Gly	Gln	Pro	Ser	265	Met	Gly	Ile	Asp	Ile	Ala	Ser	Ala		
Pro	Ala	Leu	275	Gln	Gln	Tyr	Arg	280	Thr	Ser	Ala	Gly	Ser	Pro	Ala	Asn	Gln	
Ser	Pro	Thr	290	Ser	Pro	Val	Ser	295	Asn	Gln	Gly	Phe	Ser	Pro	Gly	Ser	Ser	
305	Pro	Gln	His	Thr	Ser	Thr	Leu	310	Gly	Ser	Val	Phe	Gly	Asp	Ala	Tyr	Tyr	
				325				330										
Glu	Gln	Gln	Met	340	Ala	Ala	Arg	Gln	Ala	Asn	Ala	Leu	Ser	His	Gln	Leu		
Glu	Gln	Phe	Asn	345	Met	Met	Glu	Asn	Ala	Ile	Ser	Ser	Ser	Ser	Leu	Tyr		
Ser	Pro	Gly	Ser	355	Thr	Leu	Asn	360	Tyr	Ser	Gln	Ala	Ala	Met	Met	Gly	Leu	
Thr	Gly	Ser	His	370	Gly	Ser	Leu	375	Pro	Asp	Ser	Gln	Gln	Leu	Gly	Tyr	Ala	
385	Ser	His	Ser	390	Gly	Ile	Pro	Asn	Ile	Ile	Leu	Thr	Val	Thr	Gly	Glu	Ser	
				405				410										
Pro	Pro	Ser	Leu	420	Ser	Lys	Glu	Leu	Thr	Ser	Ser	Leu	Ala	Gly	Val	Gly		
Asp	Val	Ser	Phe	425	Asp	Ser	Asp	Ser	Gln	Phe	Pro	Leu	Asp	Glu	Leu	Lys		
Ile	Asp	Pro	Leu	435	Thr	Leu	Asp	440	Gly	Leu	His	Met	Leu	Asn	Asp	Pro	Asp	
Met	Val	Leu	Ala	445	Asp	Pro	Ala	455	Thr	Glu	Asp	Thr	Phe	Arg	Met	Asp	Arg	
465				470				475										
Leu																		

<210> 37
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 37
 caacatggcc aatccgcgca agttcagcga

30

<210> 38
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 38
 tcagttgagg tcgcgtcgaa aactatcct

29

<210> 39
 <211> 62
 <212> DNA
 <213> drosophila melanogaster

<400> 39
 ggagcctggc gtcagagagc ctggcgtcag agagcctggc gtcagagagc ctggcgtcag
 ag

60
62